SEQUENCE LISTING

<110> Afar, Daniel E.
Hubert, Rene S.
Leong, Kahan
Raitano, Arthur B.
Saffran, Douglas C.
Mitchell, Stephen C.

<120> NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS EXPRESSED IN HUMAN CANCERS AND USES THEREOF

<130> 1703-011.US1

<140> 09/323,873
<141> 1999-06-01

<150> 60/087,520
<151> 1998-06-01

<150> 60/091,183
<151> 1998-06-30

<160> 29

<170> PatentIn Ver. 2.0

<210> 1
<211> 1195
<212> DNA

<213> Homo sapiens

<400> 1
ccgagactca cggtcaagct aaggcgaaga gtgggtggct gaagccatac tattttatag 60
aattaatgga aagcagaaaa gacatcacaa accaagaaga actttggaaa atgaagccta 120
ggagaaattt agaagaagac gattatttgc ataaggacac gggagagacc agcatgctaa 180
aaagacctgt gcttttgcat ttgcaccaaa cagcccatgc tgatgaattt gactgccctt 240
cagaacttca gcacacacag gaactctttc cacagtggca cttgccaatt aaaatagctg 300
ctattatagc atctctgact tttctttaca ctcttctgag ggaagtaatt cacccttag 360
caacttccca tcaacaatat ttttataaaa ttccaatcct ggtcatcaac aaagtcttgc 420
caatggtttc catcactctc ttggcattgg tttacctgcc aggtgtgata gcagcaattg 480
tccaacttca taatggaacc aagtataaga agtttccaca ttggttggat aagtggatgt 540
taacaagaaa gcagtttggg cttctcagtt tctttttgc tgtactgcat gcaatttata 600
gtctgtctta cccaatgagg cgatcctaca gatacaagtt gctaaactgg gcatatcaac 660
aggtccaaca aaataaagaa gatgcctgga ttgagcatga tgtttggaga atggagattt 720
atgtgtctct gggaattgtg ggattggcaa tactggctct gttggctgtg acatctattc 780
catctgtgag tgactctttg acatggagag aatttcacta tattcagagc aagctaggaa 840
ttgtttccct tctactgggc acaatacacg cattgatttt tgcctggaat aagtggatag 900
atataaaaca atttgtatgg tatacacctc caacttttat gatagctgtt ttccttccaa 960
ttgttgtcct gatatttaaa agcatactat tcctgccatg cttgaggaag aagatactga 1020
agattagaca tggttgggaa gacgtcacca aaattaacaa aactgagata tgttcccagt 1080
tgtagaatta ctgtttacac acatttttgt tcaatattga tatattttat caccaacatt 1140
tcaagtttgt atttgttaat aaaatgatta ttcaaggaaa aaaaaaaaaa aaaaa 1195

<210> 2
<211> 339
<212> PRT
<213> Homo sapiens

<400> 2
Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys Met
1 5 10 15

Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
20 25 30

Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
35 40 45

Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
50 55 60

Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile
65 70 75 80

Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His
85 90 95

Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile Leu
100 105 110

Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala Leu
115 120 125

Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn Gly
130 135 140

Thr Lys Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu Thr
145 150 155 160

Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His Ala
165 170 175

Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu
180 185 190

Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp
195 200 205

Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile
210 215 220

Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser
225 230 235 240

Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser Lys
245 250 255

Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile Phe
260 265 270

Ala Trp Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr Pro
275 280 285

Pro Thr Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile Phe
290 295 300

Lys Ser Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys Ile
305 310 315 320

Arg His Gly Trp Glu Asp Val Thr Lys Ile Asn Lys Thr Glu Ile Cys
325 330 335

Ser Gln Leu

<210> 3
<211> 111
<212> DNA
<213> Homo sapiens

<400> 3
ggcggaggcg gaggcggagg gcgaggggcg gggagcgccg cctggagcgc ggcaggtcat 60
attgaacatt ccagatacct atcattactc gatgctgttg ataacagcaa g 111

<210> 4
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> RT-PCR PRIMER 8P1D4.1

<400> 4
actttgttga tgaccaggat tgga 24

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> RT-PCR PRIMER 8P1D4.2

<400> 5
cagaacttca gcacacacag gaac 24

<210> 6
<211> 3627
<212> DNA
<213> Homo sapiens

<400> 6
ggggcccgca cctctgggca gcagcggcag ccgagactca cggtcaagct aaggcgaaga 60
gtgggtggct gaagccatac tattttatag aattaatgga aagcagaaaa gacatcacaa 120
accaagaaga actttggaaa atgaagccta ggagaaattt agaagaagac gattatttgc 180
ataaggacac gggagagacc agcatgctaa aaagacctgt gcttttgcat ttgcaccaaa 240
cagcccatgc tgatgaattt gactgccctt cagaacttca gcacacacag gaactctttc 300
cacagtggca cttgccaatt aaaatagctg ctattatagc atctctgact tttctttaca 360
ctctttctgag ggaagtaatt cacccctag caacttccca tcaacaatat ttttataaaa 420
ttccaatcct ggtcatcaac aaagtcttgc caatggtttc catcactctc ttggcattgg 480
tttacctgcc aggtgtgata gcagcaattg tccaacttca taatggaacc aagtataaga 540
agtttccaca ttggttggat aagtggatgt taacaagaaa gcagtttggg cttctcagtt 600
tctttttgc tgtactgcat gcaatttata gtctgtctta cccaatgagg cgatcctaca 660
gatacaagtt gctaaactgg gcatatcaac aggtccaaca aaataaagaa gatgcctgga 720
ttgagcatga tgtttggaga atggagattt atgtgtctct gggaattgtg ggattggcaa 780
tactggctct gttggctgtg acatctattc catctgtgag tgactctttg acatggagag 840
aatttcacta tattcaggta aataatatat aaaataaccc taagaggtaa atcttctttt 900
tgtgtttatg atatagaata tgttgacttt accccataaa aaataacaaa tgtttttcaa 960
cagcaaagat cttatacttg ttccaattaa taatgtgctc tcctgttgtt ttccctattg 1020
cttctaatta ggacaagtgt ttcctagaca taaataaaag gcattaaaat attctttgtt 1080
ttttttttt tgtttgtttg ttttttgttt gtttgtttgt ttttttgaga tgaagtctcg 1140
ctctgttgcc catgctggag tacagtggca cgatctcggc tcactgcaac ctgcgcctcc 1200
tgggttcagg cgattctctt gcctcagcct cctgagtagc tgggattaca ggcacccatc 1260
accatgtcca gctaattttt gtatttttag tagagacagg gttttcccat gttggccagg 1320
ctggtctcga tctcctgacc tcaaatgatc cgcccacctc ggcctcccaa agtgctggga 1380
tgacagttgt gagccaccac actcagcctg ctctttctaa tatttgaaac ttgttagaca 1440
atttgctacc catctaatgt gatattttag gaatccaata tgcatggttt attatttctt 1500
aaaaaaaata ttcttttacc tgtcacctga atttagtaat gccttttatg ttacacaact 1560
tagcactttc cagaaacaaa aactctctcc ttgaaataat agagttttta tctaccaaag 1620
atatgctagt gtctcatttc aaaggctgct ttttccagct tacattttat atacttactc 1680
acttgaagtt tctaaatatt cttgtaattt taaaactatc tcagatttac tgaggtttat 1740
cttctggtgg tagattatcc ataagaagag tgatgtgcca gaatcactct gggatccttg 1800
tctgacaaga ttcaaaggac taaatttaat tcagtcatga acactgccaa ttaccgttta 1860
tgggtagaca tctttggaaa tttccacaag gtcagacatt cgcaactatc ccttctacat 1920
gtccacacgt atactccaac actttattag gcatctgatt agtttggaaa gtatgcctcc 1980
atctgaatta gtccagtgtg gcttagagtt ggtacaacat tctcacagaa tttcctaatt 2040

ttgtaggttc agcctgataa ccactggagt tctttggtcc tcattaaata gctttcttca 2100
cacattgctc tgcctgttac acatatgatg aacactgctt tttagacttc attaggaatt 2160
taggactgca tcttgacaac tgagcctatt ctactatatg tacaatacct agcccataat 2220
aggtatacaa tacacatttg gtaaaactaa ttttcaacca atgacatgta tttttcaact 2280
agtaacctag aaatgtttca cttaaaatct gagaactggt tacactacaa gttaccttgg 2340
agattcatat atgaaaacgc aaacttagct atttgattgt attcactggg acttaagaat 2400
gcgcctgaat aattgtgagt tcgatttgtt ctggcaggct aatgaccatt tccagtaaag 2460
tgaatagagg tcagaagtcg tataaaagag gtgttgtcag aacaccgttg agattacata 2520
ggtgaacaac tatttttaag caactttatt tgtgtagtga caaagcatcc caatgcaggc 2580
tgaaatgttt catcacatct ctggatctct ctattttgtg cagacattga aaaaattgtt 2640
catattattt ccatgttatc agaatatttg atttttaaa aacataggcc aagttcattc 2700
acttcattat tcatttatca aaatcagagt gaatcacatt agtcgccttc acaactgata 2760
aagatcactg aagtcaaatt gatttttgct ataatcttca atctacctat atttaattga 2820
gaatctaaaa tgtacaaatc attgtgttga ttctgcagtg atcctgctat aagtaagact 2880
cagtccctga ttttaggtat cctgtgaaaa gcagaattaa gacaaataca caagagacaa 2940
agcacaaaaa ataaatatca taaggggatg aacaaaatgg tggagaaaga gtagacaaag 3000
tttttgatca cctgccttca aagaaaggct gtgaattttg ttcacttaga cagcttggag 3060
acaagaaatt acccaaaagt aaggtgagga ggataggcaa aaagagcaga aagatgtgaa 3120
tggacattgt tgagaaatgt gataggaaaa caatcataga taaaggattt ccaagcaaca 3180
gagcatatcc agatgaggta ggatgggata aactcttatt gaaccaatct tcaccaattt 3240
tgtttttctt ttgcagagca agctaggaat tgtttccctt ctactgggca caatacacgc 3300
attgattttt gcctggaata agtggataga tataaaacaa tttgtatggt atacacctcc 3360
aacttttatg atagctgttt tccttccaat tgttgtcctg atatttaaaa gcatactatt 3420
cctgccatgc ttgaggaaga agatactgaa gattagacat ggttgggaag acgtcaccaa 3480
aattaacaaa actgagatat gttcccagtt gtagaattac tgtttacaca cattttgtt 3540
caatattgat atattttatc accaacattt caagtttgta tttgttaata aaatgattat 3600
tcaaggaaaa aaaaaaaaaa aaaaaaa 3627

<210> 7
<211> 521
<212> DNA
<213> Homo sapiens

<400> 7
tgacttttac aaaattccta tagagattgt gaataaaacc ttacctatag ttgccattac 60
tttgctctcc ctagtatacc tcgcaggtct tctggcagct gcttatcaac tttattacgg 120
caccaagtat aggagatttc caccttggtt ggaaacctgg ttacagtgta gaaaacagct 180
tggattacta agtttttttct tcgctatggt ccatgttgcc tacagcctct gcttaccgat 240
gagaaggtca gagagatatt tgtttctcaa catggcttat cagcaggttc atgcaaatat 300
tgaaaactct tggaatgagg aagaagtttg gagaattgaa atgtatatct cctttggcat 360
aatgagcctt ggcttacttt ccctcctggc agtcacttct atcccttcag tgagcaatgc 420
tttaaactgg agagaattca gttttattca gtctacactt ggatatgtcg ctctgctcat 480
aagtactttc catgttttaa tttatggatg gaaacgagct t 521

<210> 8
<211> 173
<212> PRT
<213> Homo sapiens

<400> 8
Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn Lys Thr Leu Pro Ile
1 5 10 15

Val Ala Ile Thr Leu Leu Ser Leu Val Tyr Leu Ala Gly Leu Leu Ala
20 25 30

Ala Ala Tyr Gln Leu Tyr Tyr Gly Thr Lys Tyr Arg Arg Phe Pro Pro
35 40 45

Trp Leu Glu Thr Trp Leu Gln Cys Arg Lys Gln Leu Gly Leu Leu Ser
50 55 60

Phe Phe Phe Ala Met Val His Val Ala Tyr Ser Leu Cys Leu Pro Met
65 70 75 80

Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn Met Ala Tyr Gln Gln Val
85 90 95

His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu Val Trp Arg Ile
100 105 110

Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly Leu Leu Ser Leu
115 120 125

Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala Leu Asn Trp Arg
130 135 140

Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val Ala Leu Leu Ile
145 150 155 160

Ser Thr Phe His Val Leu Ile Tyr Gly Trp Lys Arg Ala
165 170

<210> 9
<211> 322
<212> DNA
<213> Homo sapiens

<400> 9
ggtcgacttt tcctttattc ctttgtcaga gatctgattc atccatatgc tagaaaccaa 60
cagagtgact tttacaaaat tcctatagag attgtgaata aaaccttacc tatagttgcc 120
attactttgc tctccctagt ataccttgca ggtcttctgg cagctgctta tcaactttat 180
tacggcacca agtataggag atttccacct tggttggaaa cctggttaca gtgtagaaaa 240
cagcttggat tactaagttg tttcttcgct atggtccatg ttgcctacag cctctgctta 300
ccgatgagaa ggtcagagag at 322

<210> 10
<211> 183
<212> DNA
<213> Homo sapiens

<400> 10
tttgcagctt tgcagatacc cagactgagc tggaactgga atttgtcttc ctattgactc 60
tacttcttta aaagcggctg cccattacat tcctcagctg tccttgcagt taggtgtaca 120
tgtgactgag tgttggccag tgagatgaag tctcctcaaa ggaaggcagc atgtgtcctt 180
ttt 183

<210> 11
<211> 448
<212> DNA
<213> Homo sapiens

<400> 11
aagaaggaga atccatttag cacctcctca gcctggctca gtgattcata tgtggctttg 60
ggaatacttg ggtttttttct gtttgtactc ttgggaatca cttctttgcc atctgttagc 120
aatgcagtca actggagaga gttccgattt gtccagtcca aactgggtta tttgaccctg 180
atcttgtgta cagcccacac cctggtgtac ggtgggaaga gattcctcag cccttcaaat 240
ctcagatggt atcttcctgc agcctacgtg ttagggctta tcattccttg cactgtgctg 300
gtgatcaagt ttgtcctaat catgccatgt gtagacaaca cccttacaag gatccgccag 360
ggctgggaaa ggaactcaaa acactagaaa aagcattgaa tggaaaatca atatttaaaa 420
caaagttcaa tttagctgga aaaaaaaa 448

<210> 12
<211> 401
<212> DNA
<213> Homo sapiens

<400> 12
ggccgcggca nccgctacga cctggtcaac ctggcagtca agcaggtctt ggccanacaa 60
gagccacctc tgggtgaagg aggaggtctg gcggatggag atctacctct ccctgggagt 120
gctggccctc ggcacgttgt ccctgctggc cgtgacctca ctgccgtcca ttgcaaactc 180
gctcaactgg agggagttca gcttcgttca gtcctcactg ggctttgtgg ccntcgtgct 240
gagcacactn cacacgctca cctacggctg gacccgcgcc ttcgaggaga gccgctacaa 300
gttctacctn cctcccacct tcacgntcac gctgctggtg ccctgcgttc gttcatcctg 360
ggccaaagcc ctgtttntac tgccttgcat tcagccgnag a 401

<210> 13
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> RT-PCR PRIMER AI139607.1

<400> 13
ttaggacaac ttgatcacca gca 23

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> RT-PCR PRIMER AI139607.2

<400> 14
tgtccagtcc aaactgggtt attt 24

<210> 15
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> RT-PCR PRIMER R80991.1

<400> 15

agggagttca gcttcgttca gtc 23

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> RT-PCR PRIMER R80991.2

<400> 16
ggtagaactt gtagcggctc tcct 24

<210> 17
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> RT-PCR PRIMER 98P4B6.1

<400> 17
gactgagctg gaactggaat ttgt 24

<210> 18
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> RT-PCR PRIMER 98P4B6.2

<400> 18
tttgaggaga cttcatctca ctgg 24

<210> 19
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> STRAP-1 PEPTIDE

<220>
<223> STRAP-1 PEPTIDE

<400> 19
Arg Glu Val Ile His Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr
1 5 10 15

Lys Ile Pro Ile Leu Val
20

<210> 20
<211> 34

<212> PRT
<213> Artificial Sequence

<220>
<223> STRAP-1 PEPTIDE

<400> 20
Arg Arg Ser Tyr Arg Tyr Lys Leu Leu Asn Trp Ala Tyr Gln Gln Val
1 5 10 15

Gln Gln Asn Lys Glu Asp Ala Trp Ile Glu His Asp Val Trp Arg Met
20 25 30

Glu Ile

<210> 21
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> STRAP-1 PEPTIDE

<400> 21
Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr Pro Pro Thr Phe
1 5 10 15

<210> 22
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA SYNTHESIS PRIMER

<400> 22
ttttgtacaa gctt 14

<210> 23
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA ADAPTOR 1

<400> 23
ctaatacgac tcactatagg gctcgagcgg ccgcccgggc aggt 44

<210> 24
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA ADAPTOR 2

<400> 24 42
gtaatacgac tcactatagg gcagcgtggt cgcggccgag gt

<210> 25
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR PRIMER 1

<400> 25 22
ctaatacgac tcactatagg gc

<210> 26
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> NESTED PRIMER (NP)1

<400> 26 22
tcgagcggcc gcccgggcag gt

<210> 27
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> NESTED PRIMER (NP)2

<400> 27 20
agcgtggtcg cggccgaggt

<210> 28
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> RT-PCR PRIMER 1A

<400> 28 24
actttgttga tgaccaggat tgga

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> RT-PCR PRIMER 1B

<400> 29
cagaacttca gcacacacag gaac 24